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<140> PCT US 00/000000

<141> 2003-08-18

<150> 60/425,581

<151> 2002-11-12

<160> 23

<170> PatentIn version 3.1

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Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser
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Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala
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Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His
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Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr
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Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu
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Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg
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Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser
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Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn  
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Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys  
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Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val  
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Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile  
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His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln  
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Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu  
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Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys  
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Leu Lys Gln Glu Asn Arg Glu Ala Arg Arg Arg Ile Asp Leu Asn Leu
          20          25          30

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Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser
          35          40          45

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Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala
          50          55          60

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Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His
65          70          75          80

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Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr
          85          90          95

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Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu
          100          105          110

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Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg
          115          120          125

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Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser
          130          135          140

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Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His
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Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn  
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Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys  
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Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val  
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Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys  
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Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val  
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Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile  
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His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln  
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Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp  
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Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe  
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Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu  
340 345 350

Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp  
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Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg  
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Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu  
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Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys  
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Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser  
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Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala  
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Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His  
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Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr  
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Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu  
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Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg  
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Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser  
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Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His  
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Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn  
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Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys  
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Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val  
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Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys  
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Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val  
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Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile  
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His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln  
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Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Arg Leu Val Asp Asp Lys  
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Ala Lys Glu Arg Ser Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg  
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Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp  
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Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe  
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Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu  
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Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp  
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Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg  
370 375 380

Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu

385 390 395 400

Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys  
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Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala  
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Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His  
65 70 75 80

Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr  
85 90 95

Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu  
100 105 110

Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg  
115 120 125

Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser  
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Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His  
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Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn

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Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val	195	200	205		
Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys	210	215	220		
Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val	225	230	235	240	
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His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln	260	265	270		
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Ala Lys Asp Arg Ser Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg	290	295	300		
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Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe	325	330	335		
Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu	340	345	350		
Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp	355	360	365		
Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg	370	375	380		
Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu	385	390	395	400	

Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys  
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Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser  
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Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala  
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Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His  
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Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr  
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Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu  
100 105 110

Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg  
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Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn  
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Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys  
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Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val  
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Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys  
210 215 220

Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val  
225 230 235 240

Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile  
245 250 255

His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln  
260 265 270

Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Arg Leu Val Asp Glu Lys  
275 280 285

Ala Lys Glu Arg Ser Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg  
290 295 300

Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp  
305 310 315 320

Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe  
325 330 335

Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu  
340 345 350

Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp  
355 360 365

Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg  
370 375 380

Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu  
385 390 395 400

Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys  
405 410 415

Thr Glu Ser Pro Arg Thr Ser Gly Val Leu Ser Gln Pro His Leu Pro  
420 425 430

Phe Phe Arg  
435

<210> 11  
<211> 1308  
<212> DNA  
<213> Mus musculus

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cccattattg tgatcactct aagccctgct cctgccccgt cccagcgagc agccctgcaa 180  
ctcccactgg ccaacgatgg gggcagccgc tcaccatcct cagagagctc cccacagcac 240  
cctacacccc ccacccggcc ccgccacatg ctgggggtcc catcaacctt gttcacaccg 300  
cgcagtatgg agagcatcga gattgaccag aagctgcagg agatcatgaa gcagacaggg 360  
tacctgacta tcggggggcca gcgttatcag gcagaaatca atgacttggga gaacttgggt 420  
gagatgggca gtggtacctg tggtcagggt tggaagatgc gggtccggaa gacaggccac 480  
atcattgctg ttaagcaaat gcggcgctct gggaacaagg aagagaataa gcgcattttg 540  
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aagctgaaga aacgaatgca gggccccatt ccagagcgaa tcctgggcaa gatgactgtg 720  
gcgattgtga aagcactgta ctatctgaag gagaagcatg gcgtcatcca tcgcgatgtc 780  
aaaccctcca acatcctgct agatgagcgg ggccagatca agctctgtga ctttggcatc 840  
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tgcaagacgg actttgaggt cctcaccaaa gtcctacagg aagagcccc actcctgcct 1080  
ggtcacatgg gcttctcagg ggacttcag tcatttgtca aagactgcct tactaaagat 1140



cacaggaaga gaccaaagta taataagcta cttgaacaca gcttcatcaa gcactatgag 1200  
ataactcgagg tggatgtcgc gtcctgggtt aaggatgtca tggcgaagac cgagtcccca 1260  
aggactagtg gagtcctgag tcagcaccat ctgcccttct tcaggtag 1308

<210> 12  
<211> 435  
<212> PRT  
<213> Mus musculus

<400> 12

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Leu Lys Gln Glu Asn Arg Glu Ala Arg Arg Arg Ile Asp Leu Asn Leu  
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Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser  
35 40 45

Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala  
50 55 60

Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His  
65 70 75 80

Pro Thr Pro Pro Thr Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr  
85 90 95

Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu  
100 105 110

Gln Glu Ile Met Lys Gln Thr Gly Tyr Leu Thr Ile Gly Gly Gln Arg  
115 120 125

Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser  
130 135 140

Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His  
145 150 155 160

Ile Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn  
165 170 175

Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys  
180 185 190

Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val  
195 200 205

Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys  
210 215 220

Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val  
225 230 235 240

Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile  
245 250 255

His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln  
260 265 270

Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Arg Leu Val Asp Ser Lys  
275 280 285

Ala Lys Thr Arg Ser Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg  
290 295 300

Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp  
305 310 315 320

Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe  
325 330 335

Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu  
340 345 350

Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp  
355 360 365

Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg  
370 375 380

Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys His Tyr Glu  
385 390 395 400

Ile Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys  
405 410 415

Thr Glu Ser Pro Arg Thr Ser Gly Val Leu Ser Gln His His Leu Pro  
420 425 430

Phe Phe Arg  
435

<210> 13  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 13  
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<210> 14  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 14  
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<210> 15  
<211> 156  
<212> DNA  
<213> Human

<400> 15  
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aaccgggagg cccggcggag gatcgacctc aacctggata tcagccccca gcggcccagg 120

cccattattg tgatcactct aagccctgct cctgcc 156

<210> 16  
<211> 48  
<212> DNA  
<213> Human

<400> 16  
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<210> 17  
 <211> 435  
 <212> PRT  
 <213> Human

<220>  
 <221> MISC\_FEATURE  
 <222> (291)..(291)  
 <223> Xaa is Aspartic Acid, Glutamic Acid, or Threonine

<220>  
 <221> MISC\_FEATURE  
 <222> (293)..(293)  
 <223> Xaa is Aspartic Acid, Glutamic Acid, or Serine

<220>  
 <221> MISC\_FEATURE  
 <222> (287)..(287)  
 <223> Xaa is Aspartic Acid, Glutamic Acid, or Serine

<400> 17

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Leu Lys Gln Glu Asn Arg Glu Ala Arg Arg Arg Ile Asp Leu Asn Leu  
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Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser  
 35 40 45

Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala  
 50 55 60

Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His  
 65 70 75 80

Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr  
 85 90 95

Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu  
 100 105 110

Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg  
 115 120 125

Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser  
130 135 140

Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His  
145 150 155 160

Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn  
165 170 175

Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys  
180 185 190

Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val  
195 200 205

Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys  
210 215 220

Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val  
225 230 235 240

Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile  
245 250 255

His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln  
260 265 270

Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Arg Leu Val Asp Xaa Lys  
275 280 285

Ala Lys Xaa Arg Xaa Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg  
290 295 300

Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp  
305 310 315 320

Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe  
325 330 335

Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu  
340 345 350

Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp  
355 360 365

Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg  
370 375 380

Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu  
385 390 395 400

Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys  
405 410 415

Thr Glu Ser Pro Arg Thr Ser Gly Val Leu Ser Gln Pro His Leu Pro  
420 425 430

Phe Phe Arg  
435

<210> 18  
<211> 24  
<212> DNA  
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<220>  
<223> Primer

<400> 18  
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<210> 19  
<211> 28  
<212> DNA  
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<220>  
<223> Primer

<400> 19  
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<210> 20  
<211> 1260  
<212> DNA  
<213> Human

<400> 20  
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cccaccctgc agctcccgtt ggccaacgat gggggcagcc gctcgccatc ctgagagagc 180  
tccccgcagc accccacgcc ccccgcccgg ccccgccaca tgctgggggt cccgtcaacc 240  
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gagaacttgg gcgagatggg cagcggcacc tgcggccagg tgtggaagat gcgcttccgg 420  
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cagtgccttg ggacgttcat caccaacacg gacgtcttca tcgccatgga gctcatgggc 600  
acctgcgctg agaagctcaa gaagcggatg cagggcccca tccccgagcg cattctgggc 660  
aagatgacag tggcgattgt gaaggcgctg tactacctga aggagaagca cgggtgcatc 720  
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atccggggcg acgtatggag cctgggcatc tcgctggtgg agctggcaac aggacagttt 960  
ccctacaaga actgcaagac ggactttgag gtcctcacca aagtcctaca ggaagagccc 1020  
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<210> 21  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Tag

<400> 21

Met Gly Ser Ser His His His His His Ser Ser Gly  
1 5 10

<210> 22  
<211> 1308  
<212> DNA

<213> Human

<400> 22

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cccattattg tgatcactct aagccctgct cctgccccgt cccaacgagc agccctgcag      180
ctcccgctgg ccaacgatgg gggcagccgc tcgccatcct cagagagctc cccgcagcac      240
cccacgcccc ccgcccggcc ccgccacatg ctgggggtcc cgtcaaccct gttcacaccc      300
cgcagcatgg agagcattga gattgaccag aagctgcagg agatcatgaa gcagacgggc      360
taccggacca tcggggggcca gcgctaccag gcagaaatca acgacctgga gaacttgggc      420
gagatgggca gcggcacctg cggccagggt tggaagatgc gcttccggaa gaccggccac      480
gtcattgccg ttaagcaaat gcggcgctcc gggaacaagg aggagaacaa gcgcatcctc      540
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acgttcatca ccaacacgga cgtcttcacg gccatggagc tcatgggcac ctgcgctgag      660
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cacaggaaga gaccaaagta taataagcta cttgaacaca gttcatcaa gcgctacgag     1200
acgctggagg tggacgtggc gtcctgggtc aaggatgtca tggcgaagac tgagtcaccg     1260
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<210> 23

<211> 435

<212> PRT

<213> Human

<400> 23

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Asp Ile Ser Pro Gln Arg Pro Arg Pro Ile Ile Val Ile Thr Leu Ser  
35 40 45

Pro Ala Pro Ala Pro Ser Gln Arg Ala Ala Leu Gln Leu Pro Leu Ala  
50 55 60

Asn Asp Gly Gly Ser Arg Ser Pro Ser Ser Glu Ser Ser Pro Gln His  
65 70 75 80

Pro Thr Pro Pro Ala Arg Pro Arg His Met Leu Gly Leu Pro Ser Thr  
85 90 95

Leu Phe Thr Pro Arg Ser Met Glu Ser Ile Glu Ile Asp Gln Lys Leu  
100 105 110

Gln Glu Ile Met Lys Gln Thr Gly Tyr Pro Thr Ile Gly Gly Gln Arg  
115 120 125

Tyr Gln Ala Glu Ile Asn Asp Leu Glu Asn Leu Gly Glu Met Gly Ser  
130 135 140

Gly Thr Cys Gly Gln Val Trp Lys Met Arg Phe Arg Lys Thr Gly His  
145 150 155 160

Val Ile Ala Val Lys Gln Met Arg Arg Ser Gly Asn Lys Glu Glu Asn  
165 170 175

Lys Arg Ile Leu Met Asp Leu Asp Val Val Leu Lys Ser His Asp Cys  
180 185 190

Pro Tyr Ile Val Gln Cys Phe Gly Thr Phe Ile Thr Asn Thr Asp Val  
195 200 205

Phe Ile Ala Met Glu Leu Met Gly Thr Cys Ala Glu Lys Leu Lys Lys  
210 215 220

Arg Met Gln Gly Pro Ile Pro Glu Arg Ile Leu Gly Lys Met Thr Val  
225 230 235 240

Ala Ile Val Lys Ala Leu Tyr Tyr Leu Lys Glu Lys His Gly Val Ile  
245 250 255

His Arg Asp Val Lys Pro Ser Asn Ile Leu Leu Asp Glu Arg Gly Gln  
260 265 270

Ile Lys Leu Cys Asp Phe Gly Ile Ser Gly Arg Leu Val Asp Glu Lys  
275 280 285

Ala Lys Glu Arg Glu Ala Gly Cys Ala Ala Tyr Met Ala Pro Glu Arg  
290 295 300

Ile Asp Pro Pro Asp Pro Thr Lys Pro Asp Tyr Asp Ile Arg Ala Asp  
305 310 315 320

Val Trp Ser Leu Gly Ile Ser Leu Val Glu Leu Ala Thr Gly Gln Phe  
325 330 335

Pro Tyr Lys Asn Cys Lys Thr Asp Phe Glu Val Leu Thr Lys Val Leu  
340 345 350

Gln Glu Glu Pro Pro Leu Leu Pro Gly His Met Gly Phe Ser Gly Asp  
355 360 365

Phe Gln Ser Phe Val Lys Asp Cys Leu Thr Lys Asp His Arg Lys Arg  
370 375 380

Pro Lys Tyr Asn Lys Leu Leu Glu His Ser Phe Ile Lys Arg Tyr Glu  
385 390 395 400

Thr Leu Glu Val Asp Val Ala Ser Trp Phe Lys Asp Val Met Ala Lys  
405 410 415

Thr Glu Ser Pro Arg Thr Ser Gly Val Leu Ser Gln Pro His Leu Pro  
420 425 430

Phe Phe Arg  
435